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### AMENDMENTS TO THE CLAIMS

1. (Currently amended) A computer-based method for identifying conserved peptide motifs useful as drug targets for use in a host organism, wherein said method comprises the steps of:

- i) computationally generating overlapping peptide sequences from selected organisms of length 'N',
- ii) computationally sorting the peptide sequences of length 'N' according to amino acid sequence,
- iii) computationally matching the sorted peptide sequences of length 'N' of the selected organisms to produce matched common peptide sequences,
- iv) computationally locating the matched common peptide sequences in the protein sequences of step i) to provide locations of said matched common peptide sequences and subsequently labeling the matched common peptide sequences with their origin and location;
- v) computationally joining overlapping common peptide sequences to obtain extended conserved peptide sequences; and
- vi) comparing said extended conserved peptide sequences obtained in step (v) to host organism protein sequences to determine which of said conserved peptide sequences are not present in host proteins, wherein said conserved peptide sequences which are not present in host proteins are useful as drug targets.

2. (Previously presented) The method of claim 1, wherein 'N' is at least 4.

3. (Previously presented) The method of claim 1 wherein the selected organisms include at least one of: *Mycoplasma pneumoniae*, *Helicobacter pylori*, *Hemophilus influenzae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Bacillus subtilis*, and *Escherichia coli*.

4. (Currently amended) The method of claim 1, wherein the extended conserved peptide motifs sequences comprise one or more of the following sequences:

1. AAQSIGEPEGTQLT (SEQ ID NO:1)
35. KMSKSKGN (SEQ ID NO:35)

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2. AGDGTTTAT (SEQ ID NO:2)	36. KMSKSLGN (SEQ ID NO:36)
3. AGRHGNKG (SEQ ID NO:3)	37. KNMITGAAQMDGAIL (SEQ ID NO:37)
4. AHIDAGKTTT (SEQ ID NO:4)	38. KPNSALRK (SEQ ID NO:38)
5. CPIETPEG (SEQ ID NO:5)	39. LFGGAGVGKTV (SEQ ID NO:39)
6. DEPSIGLH (SEQ ID NO:6)	40. LGPSGCCK (SEQ ID NO:40)
7. DEPTSALD (SEQ ID NO:7)	41. LHAGGKFD (SEQ ID NO:41)
8. DEPTTALDVT (SEQ ID NO:8)	42. LIDEARTPLIISG (SEQ ID NO:42)
9. DHAGIATQ (SEQ ID NO:9)	43. LLNRAPTLH (SEQ ID NO:43)
10. DPHHGGGEG (SEQ ID NO:10)	44. LPDKAIDLIDE (SEQ ID NO:44)
11. DLGGGTFD (SEQ ID NO:11)	45. LPQKLADC (SEQ ID NO:45)
12. DVLDLWFSS (SEQ ID NO:12)	46. LSGGQQQR (SEQ ID NO:46)
13. ERERGITI (SEQ ID NO:13)	47. MGHVDHGKT (SEQ ID NO:47)
14. ERGITITSAA (SEQ ID NO:14)	48. NADFDGDQMAVH (SEQ ID NO:48)
15. ESRRIDNQLRGR (SEQ ID NO:15)	49. NGAGKSTL (SEQ ID NO:49)
16. PSGGQRQR (SEQ ID NO:16)	50. NLLGKRVD (SEQ ID NO:50)
17. GEPGVGKTA (SEQ ID NO:17)	51. NTDAEGR (SEQ ID NO:51)
18. GFDYLRDN (SEQ ID NO:18)	52. PSAVGYQPTLA (SEQ ID NO:52)
19. GHNLQEHS (SEQ ID NO:19)	53. QRVALARA (SEQ ID NO:53)
20. GIDLGTTNS (SEQ ID NO:20)	54. QRYKGLGEM (SEQ ID NO:54)
21. GINLLREGLD (SEQ ID NO:21)	55. RDGLKPVHRR (SEQ ID NO:55)
22. GIVGLPNVGKS (SEQ ID NO:22)	56. SALDVSIQA (SEQ ID NO:56)
23. GKSSLLNA (SEQ ID NO:23)	57. SGGLHGVG (SEQ ID NO:57)
24. GLTGRKIIIVDTYG (SEQ ID NO:24)	58. SGSGKSSL (SEQ ID NO:58)
25. GPPGTGKTLA (SEQ ID NO:25)	59. SGSGKSTL (SEQ ID NO:59)
26. GPPGVGKT (SEQ ID NO:26)	60. SVFAQVGERTREGND (SEQ ID NO:60)
27. GSGKTTLL (SEQ ID NO:27)	61. TGRTHQIRVH (SEQ ID NO:61)
28. GTRIFGPV (SEQ ID NO:28)	62. TGVSGSGKS (SEQ ID NO:62)
29. IDTPGHVDFT (SEQ ID NO:29)	63. TLSGGBAQRJ (SEQ ID NO:63)
30. ILAHIDHGKSTL (SEQ ID NO:30)	64. TNKYAEGYP (SEQ ID NO:64)
31. INGFGRIGR (SEQ ID NO:31)	65. TPRSNPATY (SEQ ID NO:65)
32. IREGGRTVG (SEQ ID NO:32)	66. VEGDSAGG (SEQ ID NO:66) and
33. IVGESGSGKS (SEQ ID NO:33)	67. VRKRPGMYIG (SEQ ID NO:67)
34. KFSTYATWWI (SEQ ID NO:34)	

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5. (Currently amended) The method of claim 1, further comprising increasing the number of extended conserved peptide sequences by increasing the relatedness among the organisms being compared.

6. (Currently amended) The method of any one of claims 1-4 wherein the extended conserved peptide sequences are found within the sequences of at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN  
II EXONUCLEASE ABC SUBUNIT A  
III EXONUCLEASE ABC SUBUNIT B  
IV DNA GYRASE SUBUNIT B  
V ATP SYNTHASE BETA CHAIN  
VI S-ADENOSYLMETHIONINE SYNTHETASE  
VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE  
VIII ELONGATION FACTOR G (EF-G)  
IX ELONGATION FACTOR TU (EF-TU)  
X 30S RIBOSOMAL PROTEIN S12  
XI 50S RIBOSOMAL PROTEIN L12  
XII 50S RIBOSOMAL PROTEIN L14  
XIII VALYL tRNA SYNTHETASE  
XIV CELL DIVISION PROTEIN F1SH HOMOLOG  
XV DnaK PROTEIN (HSP70)  
XVI GTP BINDING PROTEIN LepA  
~~XVII TRANSPORTER~~  
~~XVIII XVII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN~~  
OPPF.

7. (Previously presented) The method of claim 1, wherein step (iii) comprises: selecting organism names from a menu;

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iteratively comparing peptide sequences of a first organism to peptide sequences of a second organism; and, for matching sequences, writing sequences to a first file for the first organism and to a second file for the second organism.

8. (Currently amended) The method of claim 1 wherein step (iv) comprises:  
selecting protein sequences;  
iteratively comparing matched peptide sequences to protein sequences; and  
if the peptide is found in a protein sequence, labeling the peptide sequence in a file associated with the protein with: a) a protein identification number (PID), b) a location in the protein sequence, and c) a name of the selected organism.

9. (Currently amended) The method of claim 1, wherein step (v) comprises:  
iteratively comparing data peptide sequences on matched peptide locations;  
determining overlapping matched peptides; and  
determining extended peptide sequences based on overlapping matched peptide sequences.

10-12. (Canceled)